

10/29



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**RAW SEQUENCE LISTING**  
 PATENT APPLICATION: US/09/900,379

DATE: 02/06/2002  
 TIME: 09:51:06

Input Set : N:\Crf3\RULE60\09900379.raw  
 Output Set: N:\CRF3\02062002\I900379.raw

**SEQUENCE LISTING****ENTERED**

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Wong, Hing C.  
 6 Rhode, Peter R.  
 7 Widanz, Jon A.  
 8 Grammer, Susan  
 9 Edwards, Ana C.  
 10 Chavaillaz, Pierre-Andre  
 11 Jiao, Jin-An

13 (ii) TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF

15 (iii) NUMBER OF SEQUENCES: 123

17 (iv) CORRESPONDENCE ADDRESS:

18 (A) ADDRESSEE: Dade International, Inc.  
 19 (B) STREET: 1717 Deerfield Road  
 20 (C) CITY: Deerfield  
 21 (D) STATE: Illinois  
 22 (E) COUNTRY: USA  
 23 (F) ZIP: 60015

25 (v) COMPUTER READABLE FORM:

26 (A) MEDIUM TYPE: Floppy disk  
 27 (B) COMPUTER: IBM PC compatible  
 28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 29 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

31 (vi) CURRENT APPLICATION DATA:

C--> 32 (A) APPLICATION NUMBER: US/09/900,379  
 C--> 33 (B) FILING DATE: 06-Jul-2001  
 34 (C) CLASSIFICATION:

47 (vii) PRIOR APPLICATION DATA:

38 (A) APPLICATION NUMBER: US/08/776,084  
 39 (B) FILING DATE:  
 41 (A) APPLICATION NUMBER: PCT/US95/09816  
 42 (B) FILING DATE: 31-JUL-1995  
 44 (A) APPLICATION NUMBER: US 08/382,454  
 45 (B) FILING DATE: 01-FEB-1995  
 48 (A) APPLICATION NUMBER: US 08/283,302  
 49 (B) FILING DATE: 29-JUL-1994

51 (viii) ATTORNEY/AGENT INFORMATION:

52 (A) NAME: Pearson, Louise S.  
 53 (B) REGISTRATION NUMBER: 32,369  
 54 (C) REFERENCE/DOCKET NUMBER: STR-4665-CIP2

56 (ix) TELECOMMUNICATION INFORMATION:

57 (A) TELEPHONE: (708) 267-5300  
 58 (B) TELEFAX: (708) 267-5376

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Input Set : N:\Crf3\RULE60\09900379.raw  
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61 (2) INFORMATION FOR SEQ ID NO: 1:  
63 (i) SEQUENCE CHARACTERISTICS:  
64 (A) LENGTH: 10 amino acids  
65 (B) TYPE: amino acid  
66 (C) STRANDEDNESS: unknown  
67 (D) TOPOLOGY: unknown  
69 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
71 Ala Ser Gly Gly Gly Ser Gly Gly  
72 1 5 10  
74 (2) INFORMATION FOR SEQ ID NO: 2:  
76 (i) SEQUENCE CHARACTERISTICS:  
77 (A) LENGTH: 8 base pairs  
78 (B) TYPE: nucleic acid  
79 (C) STRANDEDNESS: unknown  
80 (D) TOPOLOGY: unknown  
82 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
84 CCACCATG 8  
87 (2) INFORMATION FOR SEQ ID NO: 3:  
89 (i) SEQUENCE CHARACTERISTICS:  
90 (A) LENGTH: 18 amino acids  
91 (B) TYPE: amino acid  
92 (C) STRANDEDNESS: unknown  
93 (D) TOPOLOGY: unknown  
95 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
97 Ser Ile Ser Gln Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala  
98 1 5 10 15  
100 Gly Arg  
103 (2) INFORMATION FOR SEQ ID NO: 4:  
105 (i) SEQUENCE CHARACTERISTICS:  
106 (A) LENGTH: 18 amino acids  
107 (B) TYPE: amino acid  
108 (C) STRANDEDNESS: unknown  
109 (D) TOPOLOGY: unknown  
111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
114 Ser Ile Ser Gln Ala Val His Ala Ala Arg Ala Glu Ile Asn Glu Ala  
115 1 5 10 15  
117 Gly Arg  
120 (2) INFORMATION FOR SEQ ID NO: 5:  
122 (i) SEQUENCE CHARACTERISTICS:  
123 (A) LENGTH: 18 amino acids  
124 (B) TYPE: amino acid  
125 (C) STRANDEDNESS: unknown  
126 (D) TOPOLOGY: unknown  
128 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
130 Ser Ile Ser Gln Ala Val His Ala Ala His Tyr Glu Ile Asn Glu Ala  
131 1 5 10 15  
133 Gly Arg  
136 (2) INFORMATION FOR SEQ ID NO: 6:  
138 (i) SEQUENCE CHARACTERISTICS:

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140                   (A) LENGTH: 13 amino acids  
141                   (B) TYPE: amino acid  
142                   (C) STRANDEDNESS: unknown  
143                   (D) TOPOLOGY: unknown  
145       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
147       Asn Leu Cys Asn Ile Pro Cys Ser Ala Leu Leu Ser Ser  
148       1               5                   10  
151 (2) INFORMATION FOR SEQ ID NO: 7:  
153       (i) SEQUENCE CHARACTERISTICS:  
154           (A) LENGTH: 11 amino acids  
155           (B) TYPE: amino acid  
156           (C) STRANDEDNESS: unknown  
157           (D) TOPOLOGY: unknown  
159       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
161       Gln Ile Ser Val Gln Pro Ala Phe Ser Val Gln  
162       1               5                   10  
165 (2) INFORMATION FOR SEQ ID NO: 8:  
167       (i) SEQUENCE CHARACTERISTICS:  
168           (A) LENGTH: 13 amino acids  
169           (B) TYPE: amino acid  
170           (C) STRANDEDNESS: unknown  
171           (D) TOPOLOGY: unknown  
173       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
175       Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr  
176       1               5                   10  
179 (2) INFORMATION FOR SEQ ID NO: 9:  
181       (i) SEQUENCE CHARACTERISTICS:  
182           (A) LENGTH: 13 amino acids  
183           (B) TYPE: amino acid  
184           (C) STRANDEDNESS: unknown  
185           (D) TOPOLOGY: unknown  
187       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
189       His Tyr Gly Ser Leu Pro Gln Lys Ser Gln His Gly Arg  
190       1               5                   10  
193 (2) INFORMATION FOR SEQ ID NO: 10:  
195       (i) SEQUENCE CHARACTERISTICS:  
196           (A) LENGTH: 13 amino acids  
197           (B) TYPE: amino acid  
198           (C) STRANDEDNESS: unknown  
199           (D) TOPOLOGY: unknown  
201       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
203       His Ser Leu Gly Lys Trp Leu Gly His Pro Asp Lys Phe  
204       1               5                   10  
207 (2) INFORMATION FOR SEQ ID NO: 11:  
209       (i) SEQUENCE CHARACTERISTICS:  
210           (A) LENGTH: 14 amino acids  
211           (B) TYPE: amino acid  
212           (C) STRANDEDNESS: unknown  
213           (D) TOPOLOGY: unknown

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|     |   |    |
|-----|---|----|
| 215 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:               |    |
| 217 | Met Ala Ser Gln Lys Arg Pro Ser Gln Arg Ser Lys Tyr Leu |    |
| 218 | 1                   5                   10              |    |
| 221 | (2) INFORMATION FOR SEQ ID NO: 12:                      |    |
| 223 | (i) SEQUENCE CHARACTERISTICS:                           |    |
| 224 | (A) LENGTH: 27 base pairs                               |    |
| 225 | (B) TYPE: nucleic acid                                  |    |
| 226 | (C) STRANDEDNESS: unknown                               |    |
| 227 | (D) TOPOLOGY: unknown                                   |    |
| 229 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:               |    |
| 231 | GCAGAAGAAAT TCGAGCTCGG CCCCCAG                          | 27 |
| 234 | (2) INFORMATION FOR SEQ ID NO: 13:                      |    |
| 236 | (i) SEQUENCE CHARACTERISTICS:                           |    |
| 237 | (A) LENGTH: 33 base pairs                               |    |
| 238 | (B) TYPE: nucleic acid                                  |    |
| 239 | (C) STRANDEDNESS: unknown                               |    |
| 240 | (D) TOPOLOGY: unknown                                   |    |
| 242 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:               |    |
| 244 | GATGATATCA GAGAGAAATA CATACTAACACAC                     | 33 |
| 247 | (2) INFORMATION FOR SEQ ID NO: 14:                      |    |
| 249 | (i) SEQUENCE CHARACTERISTICS:                           |    |
| 250 | (A) LENGTH: 30 base pairs                               |    |
| 251 | (B) TYPE: nucleic acid                                  |    |
| 252 | (C) STRANDEDNESS: unknown                               |    |
| 253 | (D) TOPOLOGY: unknown                                   |    |
| 255 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:               |    |
| 257 | CGGAAGAAAG AGACTTCGGC CGCTACTTAC                        | 30 |
| 260 | (2) INFORMATION FOR SEQ ID NO: 15:                      |    |
| 262 | (i) SEQUENCE CHARACTERISTICS:                           |    |
| 263 | (A) LENGTH: 47 base pairs                               |    |
| 264 | (B) TYPE: nucleic acid                                  |    |
| 265 | (C) STRANDEDNESS: unknown                               |    |
| 266 | (D) TOPOLOGY: unknown                                   |    |
| 268 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:               |    |
| 270 | GTGTGTTAGT ATGTATTCT CTCTGATATC TTCAGCTTCC AGCAGTG      | 47 |
| 273 | (2) INFORMATION FOR SEQ ID NO: 16:                      |    |
| 275 | (i) SEQUENCE CHARACTERISTICS:                           |    |
| 276 | (A) LENGTH: 21 base pairs                               |    |
| 277 | (B) TYPE: nucleic acid                                  |    |
| 278 | (C) STRANDEDNESS: unknown                               |    |
| 279 | (D) TOPOLOGY: unknown                                   |    |
| 281 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:               |    |
| 283 | TCTTCTAGAA GACCACGCTA C                                 | 21 |
| 286 | (2) INFORMATION FOR SEQ ID NO: 17:                      |    |
| 288 | (i) SEQUENCE CHARACTERISTICS:                           |    |
| 289 | (A) LENGTH: 36 base pairs                               |    |
| 290 | (B) TYPE: nucleic acid                                  |    |
| 291 | (C) STRANDEDNESS: unknown                               |    |
| 292 | (D) TOPOLOGY: unknown                                   |    |

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|     |   |    |
|-----|---|----|
| 294 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:           |    |
| 296 | GATGATATCC GGCGAAGTC TCTTCTTCC GTTGTC               | 36 |
| 299 | (2) INFORMATION FOR SEQ ID NO: 18:                  |    |
| 301 | (i) SEQUENCE CHARACTERISTICS:                       |    |
| 302 | (A) LENGTH: 24 base pairs                           |    |
| 303 | (B) TYPE: nucleic acid                              |    |
| 304 | (C) STRANDEDNESS: unknown                           |    |
| 305 | (D) TOPOLOGY: unknown                               |    |
| 307 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:           |    |
| 309 | CAGGGTTATC AACACCTGA AAAC                           | 24 |
| 311 | (2) INFORMATION FOR SEQ ID NO: 19:                  |    |
| 313 | (i) SEQUENCE CHARACTERISTICS:                       |    |
| 314 | (A) LENGTH: 21 base pairs                           |    |
| 315 | (B) TYPE: nucleic acid                              |    |
| 316 | (C) STRANDEDNESS: unknown                           |    |
| 317 | (D) TOPOLOGY: unknown                               |    |
| 319 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:           |    |
| 321 | GTCACAGTTA TCCACTCTGT C                             | 21 |
| 324 | (2) INFORMATION FOR SEQ ID NO: 20:                  |    |
| 326 | (i) SEQUENCE CHARACTERISTICS:                       |    |
| 327 | (A) LENGTH: 38 base pairs                           |    |
| 328 | (B) TYPE: nucleic acid                              |    |
| 329 | (C) STRANDEDNESS: unknown                           |    |
| 330 | (D) TOPOLOGY: unknown                               |    |
| 332 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:           |    |
| 334 | CCGTCTCCTC AGGTACGGCC GGCCTCTCCA GGTCTTCG           | 38 |
| 339 | (2) INFORMATION FOR SEQ ID NO: 21:                  |    |
| 341 | (i) SEQUENCE CHARACTERISTICS:                       |    |
| 342 | (A) LENGTH: 39 base pairs                           |    |
| 343 | (B) TYPE: nucleic acid                              |    |
| 344 | (C) STRANDEDNESS: unknown                           |    |
| 345 | (D) TOPOLOGY: unknown                               |    |
| 347 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:           |    |
| 349 | CACAGTTATC CACTCTGTCT TTGATATCAC AGGTGCCT           | 39 |
| 352 | (2) INFORMATION FOR SEQ ID NO: 22:                  |    |
| 354 | (i) SEQUENCE CHARACTERISTICS:                       |    |
| 355 | (A) LENGTH: 13 amino acids                          |    |
| 356 | (B) TYPE: amino acid                                |    |
| 357 | (C) STRANDEDNESS: unknown                           |    |
| 358 | (D) TOPOLOGY: unknown                               |    |
| 360 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:           |    |
| 362 | His Ser Leu Gly Lys Tyr Leu Gly His Pro Asp Lys Phe |    |
| 363 | 1 5 10  |    |
| 366 | (2) INFORMATION FOR SEQ ID NO: 23:                  |    |
| 368 | (i) SEQUENCE CHARACTERISTICS:                       |    |
| 369 | (A) LENGTH: 13 amino acids                          |    |
| 370 | (B) TYPE: amino acid                                |    |
| 371 | (C) STRANDEDNESS: unknown                           |    |
| 372 | (D) TOPOLOGY: unknown                               |    |

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/900,379

DATE: 02/06/2002

TIME: 09:51:07

Input Set : N:\Crf3\RULE60\09900379.raw  
Output Set: N:\CRF3\02062002\I900379.raw

L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:1888 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1892 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1896 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1900 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1904 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1908 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1912 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1916 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1920 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1925 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1929 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1933 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1937 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1941 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1945 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1949 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1953 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1957 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1961 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1965 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1969 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1973 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1977 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1981 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1985 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1990 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1994 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1998 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:2002 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:2006 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:2010 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:2014 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:2035 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2039 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2043 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2047 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2051 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2056 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2060 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2064 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2068 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2072 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2076 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2080 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2084 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2088 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123

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Input Set : N:\Crf3\RULE60\09900379.raw  
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L:2092 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2096 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2100 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2104 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123